```
1    AGCAGACAGAGGACTCTCATTAAGGAAGG TGTCCTGTGCCCTGACCCTACAAGATGCCA   59
                                                          MetPro     2

60   AGAGAAGATGCTCACTTCATCTATGGTTAC CCCAAGAAGGGGCACGGCCACTCTTACACC  119
3    ArgGluAspAlaHisPheIleTyrGlyTyr ProLysLysGlyHisGlyHisSerTyrThr   22

120  ACGGCTGAAGAGGCCGCTGGGATCGGCATC CTGACAGTGATCCTGGGAGTCTTACTGCTC  180
23   ThrAlaGluGluAlaAlaGlyIleGlyIle LeuThrValIleLeuGlyValLeuLeuLeu   43

181  ATCGGCTGTTGGTATTGTAGAAGACGAAAT GGATACAGAGCCTTGATGGATAAAAGTCTT  239
44   IleGlyCysTrpTyrCysArgArgArgAsn GlyTyrArgAlaLeuMetAspLysSerLeu   62

240  CATGTTGGCACTCAATGTGCCTTAACAAGA AGATGCCCACAAGAAGGGTTTGATCATCGG  300
63   HisValGlyThrGlnCysAlaLeuThrArg ArgCysProGlnGluGlyPheAspHisArg   83

301  GACAGCAAAGTGTCTCTTCAAGAGAAAAAC TGTGAACCTGTGGTTCCCAATGCTCCACCT  359
84   AspSerLysValSerLeuGlnGluLysAsn CysGluProValValProAsnAlaProPro  102

360  GCTTATGAGAAACTCTCTGCAGAACAGTCA CCACCACCTTATTCACCTTAAGAGCCAGCG  420
103  AlaTyrGluLysLeuSerAlaGluGlnSer ProProProTyrSerPro              118

421  AGACACCTGAGACATGCTGAAATTATTTCT CTCACACTTTTGCTTGAATTTAATACAGAC  479
```

FIG. 1A

480 ATCTAATGTTCTCCTTTGGAATGGTGTAGG AAAAATGCAAGCCATCTCTAATAATAAGTC 540
541 AGTGTTAAAATTTTAGTAGGTCCGCTAGCA GTACTAATCATGTGAGGAAATGATGAGAAA 599
600 TATTAAATTGGGAAAACTCCATCAATAAAT GTTGCAATGCATGATACTATCTGTGCCAGA 660
661 GGTAATGTTAGTAAATCCATGGTGTTATTT TCTGAGAGACAGAATTCAAGTGGGTATTCT 719
720 GGGGCCATCCAATTTCTCTTTACTTGAAAT TTGGCTAATAACAAACTAGTCAGGTTTTCG 780
781 AACCTTGACCGACATGAACTGTACACAGAA TTGTTCCAGTACTATGGAGTGCTCACAAAG 839
840 GATACTTTTACAGGTTAAGACAAAGGGTTG ACTGGCCTATTTATCTGATCAAGAACATGT 900
901 CAGCAATGTCTCTTTGTGCTCTAAAATTCT ATTATACTACAATAATATATTGTAAAGATC 959
960 CTATAGCTCTTTTTTTTTGAGATGGAGTTT CGCTTTTGTTGCCCAGGCTGGAGTGCAATG 1020
1021 GCGCGATCTTGGCTCACCATAACCTCCGCC TCCCAGGTTCAAGCAATTCTCCTGCCTTAG 1079
1080 CCTCCTGAGTAGCTGGGATTACAGGCGTGC GCCACTATGCCTGACTAATTTTGTAGTTTT 1140
1141 AGTAGAGACGGGGGTTTCTCCATGTTGGTCA GGCTGGTCTCAAACTCCTGACCTCAGGTGA 1199
1200 TCTGCCCGCCTCAGCCTCCCAAAGTGCTGG AATTACAGGCGTGAGCCACCACGCCTGGCT 1260
1261 GGATCCTATATCTTAGGTAAGACATATAAC GCAGTCTAATTACATTTCACTTCAAGGCTC 1319
1320 AATGCTATTCTAACTAATGACAAGTATTTT CTACTAAACCAGAAATTGGTAGAAGGATTT 1380
1381 AAATAAGTAAAAGCTACTATGTACTGCCTT AGTGCTGATGCCTGTGTACTGCCTTAAATG 1439
1440 TACCTATGGCAATTTAGCTCTCTTGGGTTC CCAAATCCCTCTCACAAGAATGTGCAGAAG 1500
1501 AAATCATAAAGGATCAGAGATTCTGAAAAA AAAAAAAAAAAAAAAAAAAAAAAAAAAA 1559

FIG. 1B

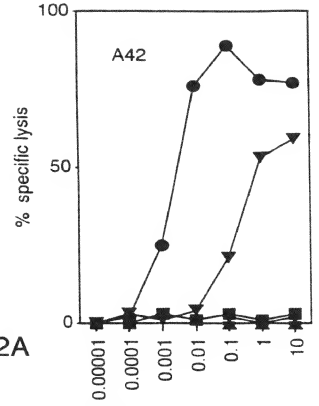
100
A42
% specific lysis
50
0
0.00001
0.0001
0.001
0.01
0.1
1
10
Peptide concentration (ug/ml)

FIG. 2A

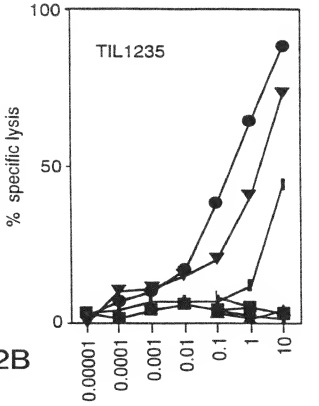
100
TIL1235
% specific lysis
50
0
0.00001
0.0001
0.001
0.01
0.1
1
10
Peptide concentration (ug/ml)

FIG. 2B

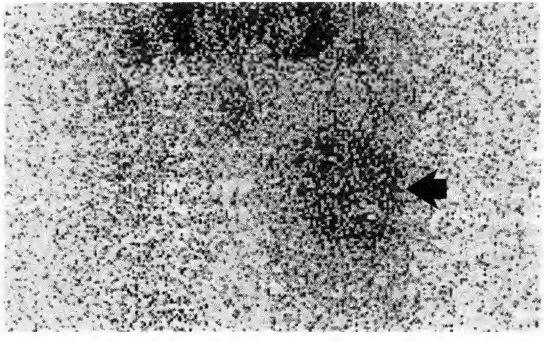

FIG. 3A

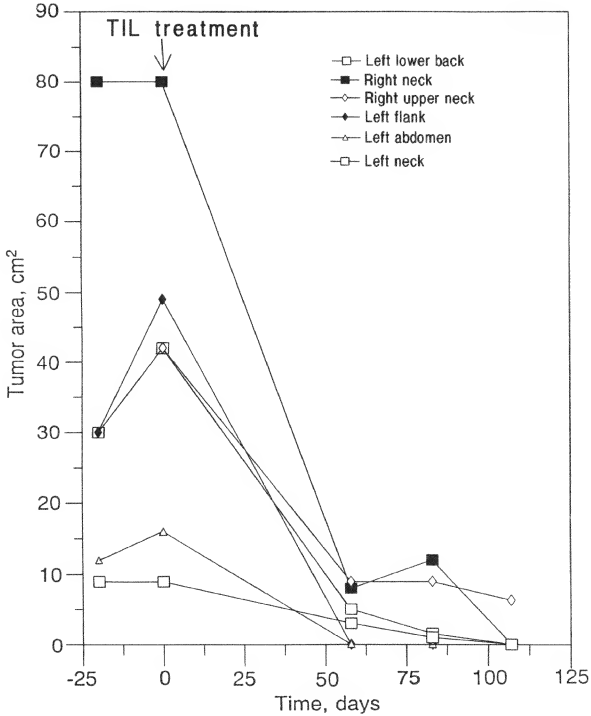
TIL treatment
Left lower back
Right neck
Right upper neck
Left flank
Left abdomen
Left neck
Tumor area, cm2
Time, days
90
80
70
60
50
40
30
20
10
0
-25
0
25
50
75
100
125

FIG. 3B

GTCGACGGCC ATTACCAATC GCGACCGGGA AGAACACAAT 40

GGATCTGGTG CTAAAAAGAT GCCTTCTTCA TTTGGCTGTG 80

ATAGGTGCTT TGCTGGCTGT GGGGGCTACA AAAGTACCCA 120

GAAACCAGGA CTGGCTTGGT GTCTCAAGGC AACTCAGAAC 160

CAAAGCCTGG AACAGGCAGC TGTATCCAGA GTGGACAGAA 200

GCCCAGAGAC TTGACTGCTG GAGAGGTGGT CAAGTGTCCC 240

TCAAGGTCAG TAATGATGGG CCTACACTGA TTGGTGCAAA 280

TGCCTCCTTC TCTATTGCCT TGAACTTCCC TGGAAGCCAA 320

AAGGTATTGC CAGATGGGCA GGTTATCTGG GTCAACAATA 360

CCATCATCAA TGGGAGCCAG GTGTGGGGAG GACAGCCAGT 400

GTATCCCCAG GAAACTGACG ATGCCTGCAT CTTCCCTGAT 440

GGTGGACCTT GCCCATCTGG CTCTTGGTCT CAGAAGAGAA 480

GCTTTGTTTA TGTCTGGAAG ACCTGGGGCC AATACTGGCA 520

ATTTCTAGGG GGCCCAGTGT CTGGGCTGAG CATTGGGACA 560

GGCAGGGCAA TGCTGGGCAC ACACACCATG GAAGTGACTG 600

TCTACCATCG CCGGGGATCC CGGAGCTATG TGCCTCTTGC 640

TCATTCCAGC TCAGCCTTCA CCATTACTGA CCAGGTGCCT 680

TTCTCCGTGA GCGTGTCCCA GTTGCGGGCC TTGGATGGAG 720

GGAACAAGCA CTTCCTGAGA AATCAGCCTC TGACCTTTGC 760

CCTCCAGCTC CATGACCCCA GTGGCTATCT GGCTGAAGCT 800

GACCTCTCCT ACACCTGGGA CTTTGGAGAC AGTAGTGGAA 840

CCCTGATCTC TCGGGCACTT GTGGTCACTC ATACTTACCT 880

GGAGCCTGGC CCAGTCACTG CCCAGGTGGT CCTGCAGGCT 920

GCCATTCCTC TCACCTCCTG TGGCTCCTCC CCAGTTCCAG 960

GCACCACAGA TGGGCACAGG CCAACTGCAG AGGCCCCTAA 1000

CACCACAGCT GGCCAAGTGC CTACTACAGA AGTTGTGGGT 1040

ACTACACCTG GTCAGGCGCC AACTGCAGAG CCCTCTGGAA 1080

CCACATCTGT GCAGGTGCCA ACCACTGAAG TCATAAGCAC 1120

FIG. 4A

TGCACCTGTG CAGATGCCAA CTGCAGAGAG CACAGGTATG 1160

ACACCTGAGA AGGTGCCAGT TTCAGAGGTC ATGGGTACCA 1200

CACTGGCAGA GATGTCAACT CCAGAGGCTA CAGGTATGAC 1240

ACCTGCAGAG GTATCAATTG TGGTGCTTTC TGGAACCACA 1280

GCTGCACAGG TAACAACTAC AGAGTGGGTG GAGACCACAG 1320

CTAGAGAGCT ACCTATCCCT GAGCCTGAAG GTCCAGATGC 1360

CAGCTCAATC ATGTCTACGG AAAGTATTAC AGGTTCCCTG 1400

GGCCCCCTGC TGGATGGTAC AGCCACCTTA AGGCTGGTGA 1440

AGAGACAAGT CCCCCTGGAT TGTGTTCTGT ATCGATATGG 1480

TTCCTTTTCC GTCACCCTGG ACATTGTCCA GGGTATTGAA 1520

AGTGCCGAGA TCCTGCAGGC TGTGCCGTCC GGTGAGGGGG 1560

ATGCATTTGA GCTGACTGTG TCCTGCCAAG GCGGGCTGCC 1600

CAAGGAAGCC TGCATGGAGA TCTCATCGCC AGGGTGCCAG 1640

CCCCCTGCCC AGCGGCTGTG CCAGCCTGTG CTACCCAGCC 1680

CAGCCTGCCA GCTGGTTCTG CACCAGATAC TGAAGGGTGG 1720

CTCGGGGACA TACTGCCTCA ATGTGTCTCT GGCTGATACC 1760

AACAGCCTGG CAGTGGTCAG CACCCAGCTT ATCATGCCTG 1800

GTCAAGAAGC AGGCCTTGGG CAGGTTCCGC TGATCGTGGG 1840

CATCTTGCTG GTGTTGATGG CTGTGGTCCT TGCATCTCTG 1880

ATATATAGGC GCAGACTTAT GAAGCAAGAC TTCTCCGTAC 1920

CCCAGTTGCC ACATAGCAGC AGTCACTGGC TGCGTCTACC 1960

CCGCATCTTC TGCTCTTGTC CCATTGGTGA GAACAGCCCC 2000

CTCCTCAGTG GGCAGCAGGT CTGAGTACTC TCATATGATG 2040

CTGTGATTTT CCTGGAGTTG ACAGAAACAC CTATATTTCC 2080

CCCAGTCTTC CCTGGGAGAC TACTATTAAC TGAAATAAAT 2120

ACTCAGAGCC TGAAAAAAAA TAAAAAAAAA AAAAAAAAAA 2160

AAAAAAAAAA AA 2172

FIG. 4B

```
  1  MDLVLKRCLL HLAVIGALLA VGATKVPRNQ DWLGVSRQLR TKAWNRQLYP
 51  EWTEAQRLDC WRGGQVSLKV SNDGPTLIGA NASFSIALNF PGSQKVLPDG
101  QVIWVNNTII NGSQVWGGQP VYPQETDDAC IFPDGGPCPS GSWSQKRSFV
151  YVWKTWGQYW QFLGGPVSGL SIGTGRAMLG THTMEVTVYH RRGSRSYVPL
201  AHSSSAFTIT DQVPFSVSVS QLRALDGGNK HFLRNQPLTF ALQLHDPSGY
251  LAEADLSYTW DFGDSSGTLI SRALVVTHTY LEPGPVTAQV VLQAAIPLTS
301  CGSSPVPGTT DGHRPTAEAP NTTAGQVPTT EVVGTTPGQA PTAEPSGTTS
351  VQVPTTEVIS TAPVQMPTAE STGMTPEKVP VSEVMGTTLA EMSTPEATGM
401  TPAEVSIVVL SGTTAAQVTT TEWVETTARE LPIPEPEGPD ASSIMSTESI
451  TGSLGPLLDG TATLRLVKRQ VPLDCVLYRY GSFSVTLDIV QGIESAEILQ
501  AVPSGEGDAF ELTVSCQGGL PKEACMEISS PGCQPPAQRL CQPVLPSPAC
551  QLVLHQILKG GSGTYCLNVS LADTNSLAVV STQLIMPGQE AGLGQVPLIV
601  GILLVLMAVV LASLIYRRRL MKQDFSVPQL PHSSSHWLRL PRIFCSCPIG
651  ENSPLLSGQQ V
```

FIG. 5A

```
Pmel17      M-----V-----Q-----P-----VPGILLT-----LLSGQQV
ME20        M-----V-----Q-----L-----  .....------------
gp100       M-----V-----Q-----L-----.....------------
cDNA25FL    M-----F-----Q-----L-----.....------------
cDNA25TR                  Q-----L-----.....-----PPQWAAGLSTLI
            1     162    236    274    588          649
```

FIG. 5B

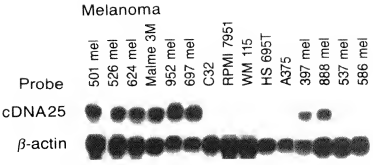

FIG. 6A

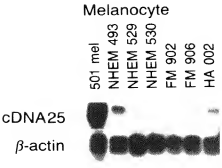

FIG. 6B

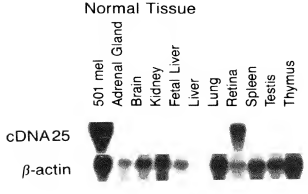

FIG. 6C